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generating template-single-stranded primer complexes. The method also includes the steps of extending each hybridized primer of said complexes by a terminating nucleotide, generating extended primers; separating the extended primers from each other and identifying each terminating nucleotide that has been added to each extended primer. Support for this claim is found, for example, on page 7, line 26 through page 8, line 12 and on page 13, line 20 through page 14, line 32.

Claim 32 is directed to a method of analyzing a nucleotide sequence of a polynucleotide of interest for the presence or absence of one or more alterations, wherein the sequence of the polynucleotide of interest is generally known. The method comprises the steps of contacting a population of single-stranded primers to said polynucleotide of interest. The population of primers comprises at least two oligonucleotides of different lengths, wherein the oligonucleotides have known sequences such that at least two oligonucleotides hybridize immediately adjacent to the one or more alterations if present, in said polynucleotide of interest, generating template-single-stranded primer complexes. The method also includes the steps of extending each hybridized primer of said complexes by a terminating nucleotide, generating extended primers; separating the extended primers from each other; identifying each terminating nucleotide that has been added to each extended primer and comparing the identified nucleotide with the sequence of the polynucleotide of interest. Support for this claim is found on page 7, line 26 through page 8, line 12. Support is also found on page 6, line 8 through line 18.

Claim 42 is drawn to a method of analyzing a nucleotide sequence of a polynucleotide of interest. The method comprises the steps of; contacting said polynucleotide of interest to a population of single-stranded primers. The single-stranded primers comprise an array of one or more sets of oligonucleotides wherein the oligonucleotides of a set differ from each other by one base at the 3' end. Said oligonucleotides have known sequence and each oligonucleotide having known sequence is attached to a solid support at a known location, forming the array. At least one oligonucleotide of the array hybridizes to said polynucleotide of interest immediately adjacent to one or more nucleotides to be identified, generating template-single-stranded primer complexes. The method also includes the steps of extending each hybridized primer of said complexes by a terminating nucleotide, generating extended primers and identifying each

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terminating nucleotide that has been added to each extended primer. Support for this claim is found on page 6, line 19 through page 7, line 12. Support is also found on page 8, line 30 through page 9, line 15 and in Figure 2.

New Claims 23-31 are ultimately dependent upon Claim 22. New Claims 33-41 are dependent upon Claim 32. New Claim 43-53 are dependent upon Claim 42. These dependent claims are essentially the same as dependent claims filed with the parent application as originally filed.

CONCLUSION

In view of the above amendments and remarks, it is believed that all claims are in condition for allowance, and it is respectfully requested that the application be passed to issue. If the Examiner feels that a telephone conference would expedite prosecution of this case, the Examiner is invited to call the undersigned at (781) 861-6240.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

By *Sandra A. Brockman*

Sandra A. Brockman

Registration No. 44,045

Telephone (781) 861-6240

Facsimile (781) 861-9540

Lexington, Massachusetts 02421-4799

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